

Spike analysis pipeline overview

Folder structure

```

^File ^Info
| Y:\Projects\project\ephys\version main folder contains:
||
| population_monkey_session.mat | spike data sorted by unit for each
session                          |
| sites_monkey_session.mat      | LFP data sorted by site for each session
|
| by_block_monkey_session.mat   | body signals sorted by block for each
session                          |
| Mon_sorted_neurons.xls        | copies of the used sorted neurons tables
from dropbox                     |
| keys_Monkey.mat               | copy of the keys used when running
ph_initiation                     |
| tuning_table_combined.mat     | Anova results stored in a table
|
| tuning_table_combined_CI.mat  | Anova results restructured accroding to
contra/ipsi definitions          |
| tuning_table_combined.xls     | simplified excel table
|
| seed.mat                      | a saved seed to make randomizations
reproducable                     |
| Subfolders:
||
| spike_shapes                  | Spike shapes, firing rates over time,
and ISI plots                    |
| single_cell_examples          | Single cell plots
|
| cell_counts                   | Anova results as pie plots
|
| scatter                       | Anova results as scatter plots (one
column versus another)          |
| population_analysis           | population PSTHs
|
| response timing               | tuning over time plots
|
| ...                           |
|
* \Dropbox\DAg\phys\Monkey_phys_dpz\Sorted_neurons excel table

```

General Workflow

- `ph_initiation(project,{version1,version2,...})`

1. loop per monkey
2. read in general settings → project settings → version settings
3. run `ph_session_processing` (core function)
 - read in data from `Y:\Data\Monkey_phys_combined_monkeypsych_TDT`
 - run `monkeypsych_analyze` for saccade detection etc.
 - run `ph_run_state_alignment_per_trial`
 1. takes over relevant trial and state (event) information
 2. combines it with Sorted Neuron table information
 3. !! Copies last 1 second of spikes to beginning of next trial
 4. !! Cuts and appends last 1 second of streams to beginning of next trial
 5. !! excludes trials without physiology data And/or NOT matching condition
 - resort data by unit/site/block
 - plot waveforms/ISI/FR_across time per unit
 - exclude units dependent on excel entries (SNR/stability/single rating)
 - plot waveforms/ISI/FR_across time per unit again for remaining units
 - run ANOVAs (`ph_ANOVAS`)
 - create single cell plots (`ph_plot_unit_per_condition`)
 - save files per session
4. format tuning table (create `tuning_table_combined_CI.mat` and `tuning_table_combined.xls`)
5. `ph_get_filelist` for crossreferencing with behavior
6. `ph_initiate_population_analysis` also runs population analysis

Synchronization

- Very important: In additi

Associated code

hmm

From:

<http://dag.dokuwiki.dpz.lokal/> - **DAG wiki**

Permanent link:

http://dag.dokuwiki.dpz.lokal/doku.php?id=spike_analysis_pipeline:pipeline_overview&rev=1641839446

Last update: **2022/12/29 07:15**

